

10/566851

SEQUENCE LISTING

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<110> Jacquemin, Marc
Saint-Remy, Jean-Marie

<120> Variable antibodies

<130> 50304/112001

<150> GB 0319118.6

<151> 2003-08-14

<150> GB 0319345.5

<151> 2003-08-18

<160> 32

<170> PatentIn version 3.3

<210> 1

<211> 496

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1) .. (495)

<223> KRIX-1 heavy chain variable region

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$$\langle 222 \rangle \quad (133) \dots (192)$$

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<222> (382) .. (435)

<223> nucleotide sequence encoding CDR3

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Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

gcc cac tcc cag gtg caa ctg gtg caa tct ggg gct gag gtg aag aag 96
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys

	20	25	30	
cct ggg gcc tca gtg aag gtc tcc tgc aag acc tct gga tac aac ttc				144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Asn Phe				
	35	40	45	
acc ggc tac tct gct tct gga cat atc ttc acc gcc tac tct gtg cac				192
Thr Gly Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His				
	50	55	60	
tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg gga agg atc				240
Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile				
	65	70	75	80
aac cct aac agt ggt gcc aca gac tat gca cat aaa ttt cag ggc agg				288
Asn Pro Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg				
	85	90	95	
gtc acc atg tcc agg gac acg tcc atc agc aca gcc tac atg gaa ctg				336
Val Thr Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu				
	100	105	110	
agc agg ctg aca tct gac gac acg gcc atg tat tac tgt gcg aga gcc				384
Ser Arg Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala				
	115	120	125	
gac aac tat ttc gat att gtg act ggc tat act tct cat tac ttt gac				432
Asp Asn Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp				
	130	135	140	
tac tgg ggc cgg gga acc ctg gtc acc gtc tcc tca gcc tcc acc aag				480
Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys				
	145	150	155	160
ggc cca tcg gtc ttc c				496
Gly Pro Ser Val Phe				
	165			

<210> 2
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 <212> PRT
 <213> Homo sapiens

<400> 2

Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
1 5 10 15

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Asn Phe
35 40 45

Thr Gly Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His
50 55 60

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile
65 70 75 80

Asn Pro Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg
85 90 95

Val Thr Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu
100 105 110

Ser Arg Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala
115 120 125

Asp Asn Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp
130 135 140

Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
145 150 155 160

Gly Pro Ser Val Phe
165

<210> 3
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<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(429)
<223> KRIX-1 light chain variable region

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<222> (1)..(60)
<223> nucleotide sequence encoding leader peptide

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<222> (130)..(164)
<223> nucleotide sequence encoding CDR1

<220>
<221> misc_feature
<222> (211)..(231)

<223> nucleotide sequence encoding CDR2

<220>

<221> misc_feature

<222> (328)..(357)

<223> nucleotide sequence encoding CDR3

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Met Glu Thr Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro	
1 5 10 15	

gat acc acc gga gaa att gtg ttg acg cag tct cca ggc acc ctg tct	96
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser	
20 25 30	

ttg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt	144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser	
35 40 45	

gtt gcc agc gcc tac tta gcc tgg tac cag caa aaa cct ggc cag gct	192
Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala	
50 55 60	

ccc agg ctc ctc atc tat ggt gca tcc agt agg gcc acc gac atc cca	240
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro	
65 70 75 80	

cac agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc	288
His Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile	
85 90 95	

agc aga ctg gag cct gaa gat ttt gca gtg tac tac tgt cag caa tat	336
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr	
100 105 110	

ggt acc tca gcc tta ctc act ttc ggc gga ggg acc aag gtg gag atc	384
Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile	
115 120 125	

aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct	429
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser	
130 135 140	

<210> 4

<211> 143

<212> PRT

<213> Homo sapiens

<400> 4

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Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser		
35	40	45
Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala		
50	55	60
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro		
65	70	75
His Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile		
85	90	95
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr		
100	105	110
Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile		
115	120	125
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser		
130	135	140

<210> 5
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Krix-1 heavy chain forward primer

<400> 5
 cggggtaccc caccatggac tggacctgga ggatc 35

<210> 6
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Krix-1 heavy chain reverse primer

<400> 6
 tatggccgac gtcgactcat ttacccggag acagggagag 40

<210> 7
 <211> 34

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Krix-1 light chain forward primer

 <400> 7
 cccaagcttc caccatggaa accccagckc agct 34

 <210> 8
 <211> 36
 <212> DNA
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 <220>
 <223> Krix-1 light chain reverse primer

 <400> 8
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 <210> 9
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Krix-1 forward mutagenic primer Asn47Gln

 <400> 9
 cctgcaagac ctctggatac caattcaccg gctactctgc ttctgg 46

 <210> 10
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Krix-1 reverse mutagenic primer Asn47Gln

 <400> 10
 ccagaagcag agtagccggt gaattggtat ccagaggtct tgcagg 46

 <210> 11
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Krix-1 forward mutagenic primer Thr49Ala

 <400> 11
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<210> 12
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 <213> Artificial Sequence

 <220>
 <223> Krix-1 reverse mutagenic primer Thr49Ala

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 <210> 13
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 <212> DNA
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 <400> 13
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 <210> 14
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 <400> 14
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 <212> DNA
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 <220>
 <223> Krix-1 forward mutagenic primer Asn47Asp

 <400> 15
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 <210> 16
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Krix-1 reverse mutagenic primer Asn47Asp

<400> 16
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<210> 17
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 17
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<210> 18
 <211> 56
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> scFv-KRIX-1VL reverse primer

<400> 18
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<210> 19
 <211> 56
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> scFv-KRIX-1VH forward primer

<400> 19
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<210> 20
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> scFv-KRIX-1VH reverse primer

<400> 20
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<210> 21
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> scFv-KRIX-1VLVH with His(6)tag forward primer

 <400> 21
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 <210> 22
 <211> 40
 <212> DNA
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 <220>
 <223> scFv-KRIX-1VLVH with His(6)tag reverse primer

 <400> 22
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 <210> 23
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> scFv- Asn47Gln KRIX-1VLVH(His) forward primer

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 <210> 24
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> scFv- Asn47Gln KRIX-1VLVH(His) reverse primer

 <400> 24
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 <210> 25
 <211> 867
 <212> DNA
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 <222> (1) .. (867)

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1 5 10 15	
gat acc acc gga gaa att gtg ttg acg cag tct cca ggc acc ctg tct	96
Asp Thr Thr Gly Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser	
20 25 30	
ttg tct cca ggg gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt	144
Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser	
35 40 45	
gtt gcc agc gcc tac tta gcc tgg tac cag caa aaa cct ggc cag gct	192
Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala	
50 55 60	
ccc agg ctc ctc atc tat ggt gca tcc agt agg gcc acc gac atc cca	240
Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro	
65 70 75 80	
cac agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc	288
His Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile	
85 90 95	
agc aga ctg gag cct gaa gat ttt gca gtg tac tac tgt cag caa tat	336
Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr	
100 105 110	
ggt acc tca gcc tta ctc act ttc ggc gga ggg acc aag gtg gag atc	384
Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile	
115 120 125	
aaa cga ggt gga ggc ggt tca ggc gga ggt ggc tct ggc ggt ggc gga	432
Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	
130 135 140	
tcg cag gta cag ctg gtg cag tct ggg gct gag gtg aag aag cct ggg	480
Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly	
145 150 155 160	
gcc tca gtg aag gtc tcc tgc aag acc tct gga tac caa ttc acc ggc	528
Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Gln Phe Thr Gly	
165 170 175	
tac tct gct tct gga cat atc ttc acc gcc tac tct gtg cac tgg gtg	576
Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His Trp Val	
180 185 190	
cga cag gcc cct gga caa ggg ctt gag tgg atg gga agg atc aac cct	624
Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile Asn Pro	
195 200 205	
aac agt ggt gcc aca gac tat gca cat aaa ttt cag ggc agg gtc acc	672
Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg Val Thr	
210 215 220	
atg tcc agg gac acg tcc atc agc aca gcc tac atg gaa ctg agc agg	720

Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg
 225 230 235 240
 ctg aca tct gac gac aca gcc atg tat tac tgt gcg aga gcc gac aac 768
 Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala Asp Asn
 245 250 255
 tat ttc gat att gtg act ggc tat act tct cat tac ttt gac tac tgg 816
 Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp Tyr Trp
 260 265 270
 ggc cgg gga acc ctg gtc acc gtc tcc tca cat cat cat cat cat cat 864
 Gly Arg Gly Thr Leu Val Thr Val Ser Ser His His His His His His
 275 280 285
 tga 867

 <210> 26
 <211> 288
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Synthetic Construct

 <400> 26

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 20 25 30
 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser
 35 40 45
 Val Ala Ser Ala Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala
 50 55 60
 Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Asp Ile Pro
 65 70 75 80
 His Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 85 90 95
 Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr
 100 105 110
 Gly Thr Ser Ala Leu Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile

115	120	125
Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly		
130	135	140
Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly		
145	150	155
Ala Ser Val Lys Val Ser Cys Lys Thr Ser Gly Tyr Gln Phe Thr Gly		
165	170	175
Tyr Ser Ala Ser Gly His Ile Phe Thr Ala Tyr Ser Val His Trp Val		
180	185	190
Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Ile Asn Pro		
195	200	205
Asn Ser Gly Ala Thr Asp Tyr Ala His Lys Phe Gln Gly Arg Val Thr		
210	215	220
Met Ser Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Arg		
225	230	235
Leu Thr Ser Asp Asp Thr Ala Met Tyr Tyr Cys Ala Arg Ala Asp Asn		
245	250	255
Tyr Phe Asp Ile Val Thr Gly Tyr Thr Ser His Tyr Phe Asp Tyr Trp		
260	265	270
Gly Arg Gly Thr Leu Val Thr Val Ser Ser His His His His His His		
275	280	285

<210> 27
 <211> 40
 <212> DNA
 <213> Artificial Sequence
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 <220>
 <223> CHO-scFvKRIX-1VLVHQ(His) forward primer
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40

<210> 28
 <211> 54

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<212> DNA
<213> Artificial Sequence

<220>
<223> CHO-scFvKRIX-1VLVHQ(His) reverse primer

<400> 28
ccggaattct caatgatgat gatgatgatg tgaggagacg gtgaccaggg ttcc 54

<210> 29
<211> 450
<212> DNA
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<220>
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<222> (1)..(450)
<223> RHD5 heavy chain variable region

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<223> nucleotide sequence encoding the leader peptide

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<222> (133)..(162)
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<222> (205)..(255)
<223> nucleotide sequence encoding CDR2

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<221> misc_feature
<222> (352)..(384)
<223> nucleotide sequence encoding CDR3

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1 5 10 15

gtc cag tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 96
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

ccc ggg tcg tcg gtg atg gtc tcc tgc aag gct tct gga ggc acc ttc 144
Pro Gly Ser Ser Val Met Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
35 40 45

agc agc ttt ggt atc agc tgg gtg cga cag gcc cct gga caa ggg ctt 192
Ser Ser Phe Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

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gag tgg gtg gga ggg atc atc cct atc ttt ggt aca gca aac acc gca 240
Glu Trp Val Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Thr Ala
65 70 75 80

aca gcc tac ata cga ctg agg agc ctg aga tct gaa gat acg gcc gtg 336
Thr Ala Tyr Ile Arg Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

gtc tgg ggc caa ggg aca atg gtc acc gtc tct tca gcc tcc acc aag 432
Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

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<210> 30
<211> 150
<212> PRT
<213> Homo sapiens
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Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Ala Gly
1 5 10 15

Pro Gly Ser Ser Val Met Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
35 40 45

Glu Trp Val Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Thr Ala
65 70 75 80

Thr Ala Tyr Ile Arg Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Val Gly Gly Arg Asp Ala Tyr Ser Phe Asp Gly Phe Asp
115 120 125

Val Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys
130 135 140

Gly Pro Ser Val Phe Pro
145 150

<210> 31
<211> 420
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(420)
<223> RHD5 light chain variable region

<220>
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<223> nucleotide sequence encoding leader peptide

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<222> (124)..(156)
<223> nucleotide sequence encoding CDR1

<220>
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<222> (202)..(222)
<223> nucleotide sequence encoding CDR2

<220>
<221> misc_feature
<222> (316)..(348)
<223> nucleotide sequence encoding CDR3

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1 5 10 15

tcc gtg gcc tcc tct ggg ctg act cag cca cac tca gtg tcc gtg tcc 96
Ser Val Ala Ser Ser Gly Leu Thr Gln Pro His Ser Val Ser Val Ser
20 25 30

cca gga cag aca gcc aac atc acc tgc tct aga gat aag ttg ggt cat 144

Pro	Gly	Gln	Thr	Ala	Asn	Ile	Thr	Cys	Ser	Arg	Asp	Lys	Leu	Gly	His		
		35					40					45					
aaa	ttt	gct	tcc	tgg	tat	caa	cag	aag	cca	ggc	cag	tcc	cct	gct	ctt	192	
Lys	Phe	Ala	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Ala	Leu		
	50					55				60							
ctc	atc	tat	caa	gac	agc	aag	cgg	ccc	tca	ggg	atc	cct	gag	cga	ttc	240	
Leu	Ile	Tyr	Gln	Asp	Ser	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe		
65					70				75					80			
tct	ggc	tcc	aac	tct	ggg	aac	aca	gcc	act	ctg	acc	atc	agc	ggg	acc	288	
Ser	Gly	Ser	Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Thr		
			85					90						95			
cag	gct	atg	gat	gag	gct	gac	tat	tac	tgt	cag	gcg	tgg	gac	aac	acc	336	
Gln	Ala	Met	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ala	Trp	Asp	Asn	Thr		
		100					105					110					
act	gcc	gta	ttc	ggc	gga	ggg	acc	aag	ttg	aca	gtc	cta	agt	cag	ccc	384	
Thr	Ala	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Ser	Gln	Pro		
	115					120					125						
aag	gct	gcc	ccc	tcg	gtc	act	ctg	ttc	ccg	ccc	tcc					420	
Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser						
	130					135					140						

<210> 32
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 32

Met	Ala	Trp	Ile	Pro	Leu	Phe	Leu	Gly	Val	Leu	Val	Tyr	Cys	Thr	Gly
1				5				10						15	

Ser	Val	Ala	Ser	Ser	Gly	Leu	Thr	Gln	Pro	His	Ser	Val	Ser	Val	Ser
		20						25					30		

Pro	Gly	Gln	Thr	Ala	Asn	Ile	Thr	Cys	Ser	Arg	Asp	Lys	Leu	Gly	His
		35					40					45			

Lys	Phe	Ala	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Ala	Leu
	50					55					60				

Leu	Ile	Tyr	Gln	Asp	Ser	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe
65					70					75					80

Ser	Gly	Ser	Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Thr
			85					90						95	

Gln	Ala	Met	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ala	Trp	Asp	Asn	Thr
			100					105					110		

Thr	Ala	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Ser	Gln	Pro
		115					120					125			

Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser
130						135					140